MOLECULAR MAPPING OF ROOT ROT RESISTANCE IN COMMON BEANS

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Introduction

Fusarium root rot, caused by *Fusarium. solani* f. sp. phaseolus , is a major disease of beans in southwestern Ontario. All currently recommended Ontario Cultivars of beans are susceptible to root rot disease complex. However, root rot resistant germplasms are available. Incorporation of genes from source germplasm to commercially grown cultivars can be accomplished through a marker assisted selection program. The present experiment was undertaken to identify molecular marker(s) linked to *Fusarium* root rot resistance in common beans. Our objectives were to determine inheritance and linkage of root resistance genes, map QTLs relative to molecular markers and map molecular markers relative to each other.

Materials and Methods

Plant Material: A cross was made between a root rot susceptible navy bean cv. AC Compass and NY2114-12, a germplasm highly resistant to *Fusarium* root rot. $F_{2:6}$ recombinant inbred lines from this cross were used as a mapping population.

Disease and Seed Trait: Three weeks after inoculation severity of root rot was visually scored using a 0-10 scale: 0 = no root rot; 1 = 1-10% of root area affected; 2 = 11 - 20% of root area affected, 3 = 21-30% of root area affected, and so on (Tu and Park 1993). Seed luster was rated using a scale of 1-5 where, 1 for very shiny and 5 for very dull. AC Compass has dull oval white seed and Ny2114-12 has elongated shiny dark brown seed. Seed shape was rated using a scale of 1-5 where 1 for round and 5 for elongated shape. Seed coat colour was rated using a scale of 1-7 where, 1 for white and 7 for dark brown.

DNA extraction and PCR: DNA extraction was done following a protocol described by Yu et al. (1999). PCR was done following a protocol described by Chowdhury et al. (2000).

Marker Analysis: RAPD markers have been used for mapping. Bulked Segregant Analysis (BSA) have been used to detect putatively linked (linked to root rot) markers. General linkage analysis was performed to detect additional linkage.

Statistical Analysis: Linkage among molecular makers was computed using MAPMAKER/EXP. The putative location of QTLs was determined using MAPMAKER/QTL. The analysis of variance for quantitative traits was performed using SAS.

Results and Discussion

Genetic control of the characteristics: The disease scores, averaged over five plants and two replications (i.e. 10 plants), were used for checking their distribution. The normal distribution of disease reaction indicated quantitative inheritance for resistance for *Fusarium* root rot (Fig 1). Analysis of variance revealed significant differences between the RILs for each trait. High broad sense heritability estimates were observed in all traits indicating less environmental influence over these traits.

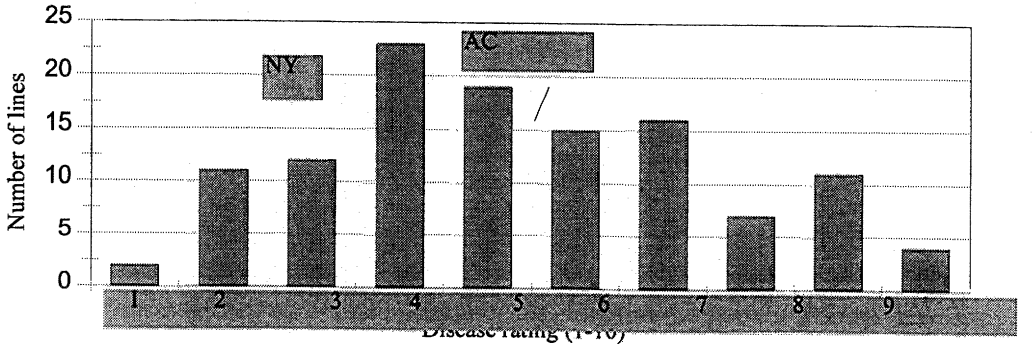

Figure 1. Frequency distribution of root rot caused by *F. solani* in a cross, AC Compass / NY2114-12, F2:6.

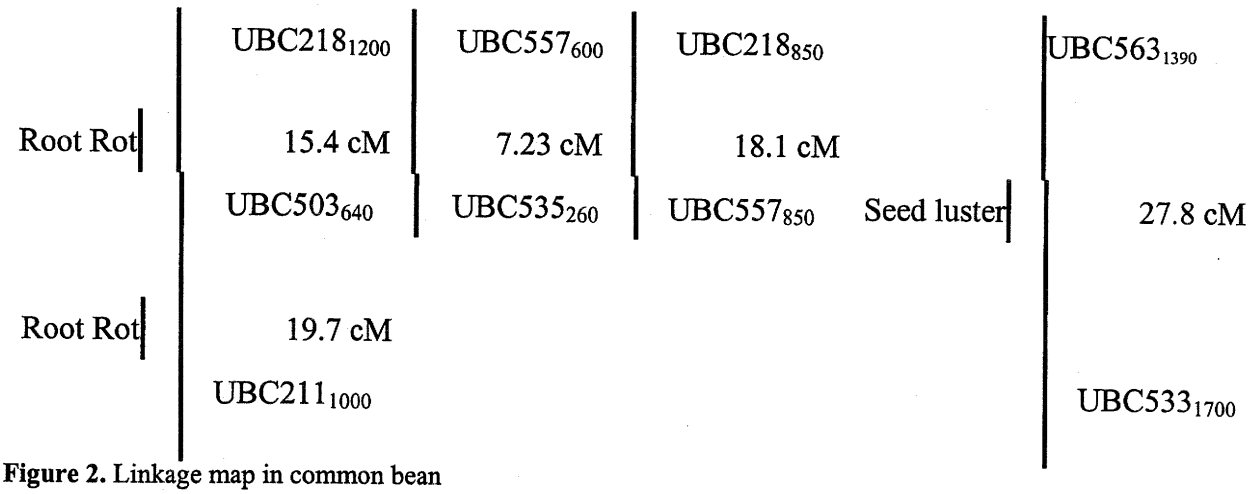

Figure 2. Linkage map in common bean

Linkage Map: After screening 400 RAPD primers two markers (UBC218$_{1200}$ and UBC503$_{640}$) were identified polymorphic between resistant and susceptible lines and parents. Two possibly linked RAPD markers along with 40 other polymorphic RAPD markers were scored for 117 individual RILs and data analysed. Out of 42 RAPD markers nine markers were linked to form four linkage groups (Fig 2) spanning a total distance of 88 cM. Linkage groups ranged from 7.2 cM to 35.1 cM with an average distance of 17.6 cM. Two markers that were polymorphic in the bulks are in the same linkage group along with a third RAPD marker UBC211$_{1000}$.

Detection of QTL: Interval mapping of QTLs revealed two QTLs for root rot resistance, one located between the markers UBC218$_{1200}$ and UBC503$_{640}$ and the other located between the markers UBC503$_{640}$ and UBC211$_{1000}$. Of two QTLs one that is located between UBC218$_{1200}$ and UBC503$_{640}$ was detected with a LOD 8.0 and explained 30% of phenotypic variation. The other QTL was detected with a LOD 5.0 and explained about 20% of phenotypic variance. Seed lustre showed one QTL located between the markers UBC563$_{1390}$ and UBC533$_{1700}$ as detected with a LOD score 2.8 and explained about 15% of phenotypic variation. In present experiment quantitative inheritance was observed for root resistance that agrees with previous results reported by Azzam (1957), Bravo et al. (1969) and Park and Rupert (2000). For root rot resistance, total phenotypic variation explained by two QTLs is about 50% indicating major effect of these two QTLs on root rot resistance. Higher heritability was observed for seed lustre, seed shape and seed coat colour indicating negligible effect of environment on these traits. Though several reference RAPD markers have been included in this experiment no linkage could be establishes with them may be due to insufficient number of polymorphic markers in this study. More polymorphic markers needed to be analyzed in this population to obtain a closer linkage between markers (<5 cM) and to obtain a more saturated linkage map in common bean.

Acknowledgement

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References

Azzam, H.A. 1957. Inheritance of resistance to Fusarium root rot in *Phaseolus vulgaris L.* and *Phaseolus coccineus* L. Ph.D. Thesis, Oregon State Univ., Corvallis.

Bravo, A., D.H., Wallace, and R.E., Wilkinson. 1969. Inheritance of resistance to Fusarium root rot of beans. Phytopathology 59:1930-1933.

Chowdhury, M.A., C.P. Andrahennadi, A.E. Slinkard and A. Vandenberg. 2000. RAPD and SCAR markers for resistance to ascochyta blight in lentil. Euphytica 118:331-337.

Park, S.J. and T. Rupert. 2000. Breeding for root rot resistance in common bean (*Phaseolus vulgaris* L.).Ann. Rep. Of the Bean Improv. Coop. 43: 41-42.

Tu, J.C., and S.J., Park. 1993. Root-rot resistance in common bean. Can. J. Plant Sci. 73:365-367.

Yu, K., S.J. Park and V. Poysa 1999. Abundance and variation of microsatellite DNA sequences in beans (Phaseolus and Vigna). Genome 42:27-34